

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/223,263DATE: 07/01/94
TIME: 13:29:35

INPUT SET: S8190.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Eaton, Dan L.
DeSavage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 4-APR-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: 871P3

ENTERED

RAW SEQUENCE LISTING PATENT APPLICATION US/08/223,263

DATE: 07/01/94
TIME: 13:29:48

INPUT SET: S8190.raw

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47
48     (ix) TELECOMMUNICATION INFORMATION:
49         (A) TELEPHONE: 415/225-1249
50         (B) TELEFAX: 415/952-9881
51         (C) TELEX: 910/371-7168
52
53     (2) INFORMATION FOR SEQ ID NO:1:
54
55         (i) SEQUENCE CHARACTERISTICS:
56             (A) LENGTH: 353 amino acids
57             (B) TYPE: amino acid
58             (D) TOPOLOGY: linear
59
60         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62     Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
63         1             5             10             15
64
65     Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
66             20             25             30
67
68     Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
69             35             40             45
70
71     Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
72             50             55             60
73
74     Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
75             65             70             75
76
77     Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
78             80             85             90
79
80     Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
81             95             100            105
82
83     Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
84             110            115            120
85
86     Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
87             125            130            135
88
89     Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
90             140            145            150
91
92     Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
93             155            160            165
94
95     Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
96             170            175            180
97
98     Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
99             185            190            195

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100
101 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
102 200 205 210
103
104 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
105 215 220 225
106
107 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
108 230 235 240
109
110 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
111 245 250 255
112
113 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
114 260 265 270
115
116 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
117 275 280 285
118
119 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
120 290 295 300
121
122 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
123 305 310 315
124
125 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
126 320 325 330
127
128 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
129 335 340 345
130
131 Ser Gln Asn Leu Ser Gln Glu Gly
132 350 353
133

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

143
144
145 TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
146
147
148 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
149
150
151 CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
152

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153
154 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
155
156
157 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
158
159
160 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGCTG 300
161
162
163 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
164
165
166 AGACTGAGCC AGTGCCCAAG GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
167
168
169 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
170
171
172 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
173
174
175 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
176
177
178 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
179
180
181 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
182
183
184 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
185
186
187 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750
188
189
190 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
191
192
193 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
194
195
196 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
197
198
199 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
200
201
202 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACCTCGT GACTCTTTCC 1000
203
204
205 TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050

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206
207
208 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100
209
210
211 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150
212
213
214 CTTGCCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200
215
216
217 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
218
219
220 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
221
222
223 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350
224
225
226 AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
227
228
229 GGGATACACA GGACTGAAAA GGGAATCATT TTTCCTGTA CATTATAAAC 1450
230
231
232 CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
233
234
235 GCTCTTTGGT CTATTTTCTG CAGAAATTG CAACTCACTG ATTCTCTACA 1550
236
237
238 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
239
240
241 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
242
243
244 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700
245
246
247 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750
248
249
250 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795
251
252
253

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/223,263

DATE: 07/01/94
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Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/223263